

## FIG. 1

-54 AGCTGCGGCCCCGGTCTGCCAGCCAGACCCTTTGGAGAAGACCCCCACTCCCTGTC  
1 ATGGGCCCCCGCTGCACCCCTGCACCCCTTTTCTCTCCTGGTGCAGGTGACAGCGCTGGCT 60  
M G P R C T L H P L S L L V Q V T A L A  
61 GCGACTCTGGCCAGGGCAGGCTGCCTGCCTTCCTGCCCTGTGAGCTCCAGCCCCACGGC 120  
A T L A Q G R L P A F L P C E L Q P H G  
121 CTGGTGAAGTGAAGTGGCTCTTCCTGAAGTCCGTGCCCCACTTCTCGGCGGCAGCGCC 180  
L V N C N W L F L K S V P H F S A A A P  
181 OGGGCCAACGTACACAGCCTCTCCTTACTCTCCAACCGCATCCACCACTTGCACGACTCT 240  
R A N V T S L S L L S N R I H H L H D S  
241 GACTTCGTCCACCTGTCCAGCCTACGAAGTCTCAACCTCAAGTGGAACTGCCCCCGGGCT 300  
D F V H L S S L R T L N L K W N C P P A  
301 GGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATGAGCCCAACACCTTCCTGGCC 360  
G L S P M H F P C H M T I E P N T F L A  
361 GTGCCACCCCTGGAGGAGCTGAACCTGAGCTACAACAGCATCACGACCGTGCCTGCCCTG 420  
V P T L E E L N L S Y N S I T T V P A L  
421 CCGACTCCCTCGTGTCCCTGTGCTGAGCGGCACCAACATCCTGGTGCTAGACCCCAAC 480  
P D S L V S L S L S R T N I L V L D P T  
481 CACCTCACTGGCCTACATGCCCTGCGCTACCTGTACATGGATGGCAACTGCTACTACAAG 540  
H L T G L H A L R Y L Y M D G N C Y Y K  
541 AACCCTGCCAGGGGGCGCTGGAGGTGGTGCCGGGTGCCCTCCTCGGCCTGGGCAACCTC 600  
N P C Q G A L E V V P G A L L G L G N L  
601 ACACATCTCTCACTCAAGTACAACAATCTCACGGAGGTGCCCGCAGCCTGCCCCCAGC 660  
T H L S L K Y N N L T E V P R S L P P S  
661 CTGGAGACCCTGCTGTTGTCTTACAACCACATTGTACCCCTGACGCTGAGGACCTGGCC 720  
L E T L L L S Y N H I V T L T P E D L A  
721 AATCTGACTGCCCTGCGCGTCTTGATGTGGGGGGGAAGTGGCGCCGCTGTGACCATGCC 780  
N L T A L R V L D V G G N C R R C D H A  
(SEQ ID NO:1 1-834)  
(SEQ ID NO:2 1-260)

## FIG. 2

781 CGCAACCCCTGCAGGGAGTGCCCAAAGGACCACCCCAAGCTGCACTCTGACACCTTCAGC 840  
R N P C R E C P K D H P K L H S D T F S  
841 CACCTGAGCCGCCCTCGAAGGCTGGTGTGAAAGACAGTTCTCTCTACAACTGGACGCC 900  
H L S R L E G L V L K D S S L Y N L D A  
901 AGGTGGTTCCGAGGCCTGGACAGGCTCCAAGTGCTGGACCTGAGTGAGAACTTCCTCTAC 960  
R W F R G L D R L Q V L D L S E N F L Y  
961 GACTGCATCACCAAGACCACGGCCTTCCAGGGCCTGGCCCCGACTgCGcAAGCTCAACCTG 1020  
D C I T K T T A F Q G L A R L R K L N L  
1021 TCCTTCAATTACCACAAGAAGGTGTCTTTGCCCCACCTGCACCTGGCACCCCTCCTTTGGG 1080  
S F N Y H K K V S F A H L H L A P S F G  
1081 CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGGCATCTTCTTCCGCTCGCTCAGTGAG 1140  
H L R S L K E L D M H G I F F R S L S E  
1141 ACCACGCTCCAACCTCTGGTCCAAGTGCCTATGCTCCAGAACCTGCGCCTGCAGATGAAC 1200  
T T L Q P L V Q L P M L Q T L R L Q M N  
1201 TTCATTAACCAGGCCACCTCAGCATCTTTGGGGCCTTCCCTGGCCTGCTGTACGTGGAC 1260  
F I N Q A Q L S I F G A F P G L L Y V D  
1261 CTATCGGACAACCGCATCAGCGAGCTGCAAGGCCAGTGGcCATTACTAGGGAGGTGGAT 1320  
L S D N R I S G A A R P V A I T R E V D  
1321 GGTAGGGAGAGGTCTGGCTGCCTTCCAGGAACCTCGCTCCACGTCCACTGGACACTCTC 1380  
G R E R V W L P S R N L A P R P L D T L  
1381 CGCTCAGAGGACTTCATGCCAAACTGCAAGGCCTTCAGCTTACCTTGGACCTGTCTCGG 1440  
R S E D F M P N C K A F S F T L D L S R  
1441 AACAACTGGTGACAATCCAGTCGGAGATGTTTGCTCGCCTCTCAGCCTCGAGTGCCTG 1500  
N N L V T I Q S E M F A R L S R L E C L  
1501 CGTCTGAGCCACAACAGCATCTCCAGGCGGTCAATGGCTCTCAGTTTGTGCCGCTGACC 1560  
R L S H N S I S Q A V N G S Q F V P L T  
(SEQ ID NO:1 835-1614)  
(SEQ ID NO:2 261-520)

## FIG. 3

1561 AGCCTGCGGGTGCTGGACCTGTCCCACAACAAGCTGGACCTGTATCACGGGCGCTCGTTC 1620  
S L R V L D L S H N K L D L Y H G R S F  
1621 ACGGAGCTGCCGCGCCTGGAAGCACTGGACCTCAGCTACAACAGCCAGCCCTTTACCATG 1680  
T E L P R L E A L D L S Y N S Q P F T M  
1681 CAGGGTGTGGGCCACAACCTCAGCTTCGTGGCCAGCTGCCCGCCCTGCGCTACCTCAGC 1740  
Q G V G H N L S F V A Q L P A L R Y L S  
1741 CTGGCGCACAATGACATCCATAGCCGAGTGTCCAGCAGCTCTGTAGCGCCTCACTGTGC 1800  
L A H N D I H S R V S Q Q L C S A S L C  
1801 GOCCTGGACTTTAGCGCAACGATCTGAGCCGATGTGGGCTGAGGGAGACCTCTATCTC 1860  
A L D F S G N D L S R M W A E G D L Y L  
1861 CGCTTCTTCCAAGGCCTAAGAAGCCTAGTCTGGCTGGACCTGTCCAGAACCACTGCAC 1920  
R F F Q G L R S L V W L D L S Q N H L H  
1921 ACCCTCCTGCCACGTGOCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT 1980  
T L L P R A L D N L P K S L K H L H L R  
1981 GACAATAACCTGGCCTTCTTCAACTGGAGCAGCCTGACCCTCCTGCCCAAGCTGGAAACC 2040  
D N N L A F F N W S S L T L L P K L E T  
2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCACC 2100  
L D L A G N Q L K A L S N G S L P S G T  
2101 CAGCTGCGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160  
Q L R R L D L S G N S I G F V N P G F F  
2161 GOCCTGGCCAAGCAGTTAGAAGAGCTCAACCTCAGCGCCAATGOCCTCAAGACAGTGGAG 2220  
A L A K Q L E E L N L S A N A L K T V E  
2221 CCCTCCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280  
P S W F G S M V G N L K V L D V S A N P  
2281 CTGCACTGCGCCTGTGGGGCGACCTTCGTGGGCTTCCTGCTGGAGGTACAGGCTGCCGTG 2340  
L H C A C G A T F V G F L L E V Q A A V  
(SEQ ID NO:1 1615-2394)  
(SEQ ID NO:2 521-780)

## FIG. 4

2341 CCTGGGCTGCCCAGCCGCGTCAAGTGTGGCAGTCCGGGGCAGCTCCAGGGCCATAGCATC 2400  
P G L P S R V K C G S P G Q L Q G H S I  
2401 TTTGCCAAGACCTGCGCCTCTGCCTGGATGAGACCTCTCGTGGAAGTGT TTTGGCATC 2460  
F A Q D L R L C L D E T L S W N C F G I  
2461 TCGCTGCTGGCCATGGGCCTGGGCTGGTTGTGCCATGCTGCACCACCTCTGCGGCTGG 2520  
S L L A M A L G L V V P M L H H L C G W  
2521 GACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTGCCCCACCGAGGGCAGCGGCGG 2580  
D L W Y C F H L C L A W L P H R G Q R R  
2581 GCGGCAGACGCCCTGTTCTATGATGCCTTCGTGGTCTTTGACAAAGCTCAGAGTGCTGTG 2640  
G A D A L F Y D A F V V F D K A Q S A V  
2641 GCGACTGGGTGTACAACGAGCTGCGGGTGACAGCTGGAGGAGCGCCGTGGGCGCCgCGCA 2700  
A D W V Y N E L R V Q L E E R R G R R A  
2701 CTGCGCCTGTGCCTGGAGGAGCGAGACTGGTTAOCCTGGCAAGACGCTCTTCGAGAACCCTG 2760  
L R L C L E E R D W L P G K T L F E N L  
2761 TGGGCCTCAGTCTACAGCAGCCGCAAGACUCTGTTTGTGCTGGGCCACACGGACCGTGTC 2820  
W A S V Y S S R K T L F V L A H T D R V  
2821 AGCGGCCTCTTGCGTGCCAGTTTCTGCTGGGCCAGCAGCGCCTGCTGGAGGACCGCAAG 2880  
S G L L R A S F L L A Q Q R L L E D R K  
2881 GACGTTGTAGTGCTGGTGATCCTGCGCCCCGATGCCTACCGCTCCCGCTACGTGCGGCTG 2940  
D V V V L V I L R P D A Y R S R Y V R L  
2941 CCGCAgCGCCTCTGCGGCCAGAGTGTCCTCCTCTGGCCCCACCAGCCCCGTGGGCAGGGC 3000  
R Q R L C R Q S V L L W P H Q P R G Q G  
3001 AGCTTCTGGGCCAGCTGGGCACAGCCTGACCAGGGACAACCGCCACTTCTATAACCGG 3060  
S F W A Q L G T A L T R D N R H F Y N R  
3061 AACTTCTGCGGGGGCCCCACGACAGCCGAATAG 3093 (SEQ ID NO:1 2395-3147)  
N F C R G P T T A E \* (SEQ ID NO:2 781-1030)

## FIG. 6

SWINE	1	MGPRT--LHPLSLLVQVTLAATLAQGRIPAFLPCELOPHGLVNCNWLFLKSVPHFSAA	58	SWINE
HUMAN	1	MGF-CRSALHPLSLLVQAIMLAMTLALGTIPAFLPCELOPHGLVNCNWLFLKSVPHFSMA	59	HUMAN
MOUSE	1	MVLRRT-LHPLSLLVQAAVLAETLALGTIPAFLPCELKPHGLVDCNWLFLKSVPRFSAA	59	MOUSE
CAT	1	MGP-CHGALHPLSLLVQAAALAVALAQGTIPAFLPCELOPHGLVNCNWLFLKSVPHFSAA	59	CAT
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SWINE	59	APRANVTLSLLSNRIHHLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTF	118	SWINE
HUMAN	60	APRGVNTLSLSSNRIHHLHDSDFVHLSSLRHLNKNCPVGLSPMHFPCHMTIEPSTF	119	HUMAN
MOUSE	60	ASCNITRLSLISNRIHHLHNSDFVHLNLRQNLKNCPPTGLSPLHFSCHMTIEPRTF	119	MOUSE
CAT	60	APRGVNTLSLSNRIHHLHDSDFVHLSSLRRNLKNCPASLSPMHFPCHMTIEPHTF	119	CAT
* . . * . * . *** ***** . *** . * . ** ***** . *** . * . ***** **				
SWINE	119	LAVPTLEEINLSYNSITTVPALPDSLVSLSLRINILVLDPTHLTGLHALRYLYMDGNCY	178	SWINE
HUMAN	120	LAVPTLEEINLSYNNIMIVPALPKSLISLSLSHTNIMLDSASLAGLHARFLFMDGNCY	179	HUMAN
MOUSE	120	LAMPTLEEINLSYNGITTVPRLPSSLVNLSSLHTNIMLDANSIAGLYSLRVLFMDGNCY	179	MOUSE
CAT	120	LAVPTLEEINLSYNSITTVPALPSSLVLSLSLRINILVLDPANLAGLSLRFELDQNCY	179	CAT
** .. ***** * . *** . ** ** .. ***** ** * . ** . ** * . *****				
SWINE	179	YKNPCQGALEVVPGALLGLGNLTHLSLKYNMLTEVPRSLPPSLETLLLSYNHIVTLTPED	238	SWINE
HUMAN	180	YKNPCRQALEVAPGALLGLGNLTHLSLKYNMLTVPRLNLPSSLEYLLLSYNRIVKLAPED	239	HUMAN
MOUSE	180	YKNPCTGAVKVTPGALLGLGNLTHLSLKYNMLTKVPRQLPPSLEYLLVSYNLIVKLPED	239	MOUSE
CAT	180	YKNPCQALQVAPGALLGLGNLTHLSLKYNMLTAVPRGLPPSLEYLLLSYNHITLAPED	239	CAT
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SWINE	239	LANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSSLYNL	298	
				(SEQ ID NO:2 1-298)
HUMAN	240	LANLTALRVLDVGGNCRRCDHAPNPMCECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWL	299	
				(SEQ ID NO:4 1-299)
MOUSE	240	LANLTSLRVLDVGGNCRRCDHAPNPMCEGQKSLHLPETFHLSHLEGLVLKDSSLHTL	299	
				(SEQ ID NO:6 1-299)
CAT	240	LANLTALRVLDVGGNCRRCDHARNPMCECPKGFPHLPDTFSHINHLEGLVLKDSSLYNL	299	
				***** . ***** ***** ** ** . ** . ** . ***** *
				(SEQ ID NO:8 1-299)



## FIG. 8

[illegible]

## FIG. 9

SWINE	838	CGNDLWYCFHLCLAWLPHRGQRRGAD--ALFYDAFVFDKAQSAVADWVYNELRVQLEER	895
HUMAN	839	CGNDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVFDKTQSAVADWVYNELRGQLEEC	898
MOUSE	840	CGNDVWYCFHLCLAWLP LLARSRRSAQA-LPYDAFVFDKAQSAVADWVYNELRVRLRGR	898
CAT	839	CGNDLWYCFHLCLAWLPRGRRRRGAD--ALPYDAFVFDKAQSAVADWVYNELRVRLRLEER	896
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SWINE	896	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQORL	955
HUMAN	899	RGRNALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQORL	958
MOUSE	899	RGRRALRLCLEERDWLPGQTLFENLWASTYGSRKTLFVLAHTDRVSGLLRTSFLLAQORL	958
CAT	897	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQORL	956
***, *****. *****. *****. * ***. *****. *****. *****			
SWINE	956	LED RKDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTDRNR	1015
HUMAN	959	LED RKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQSGQRSFWAQLGMALTDRNH	1018
MOUSE	959	LED RKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLWPHQPNQGGFWAQLSTALTDRNR	1018
CAT	957	LED RKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLWPHQSGQRSFWAQLGTALTDRNQ	1016
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SWINE	1016	HFYNRNFCRCPTTAE (SEQ ID NO:2 838-1030)	1030
HUMAN	1019	HFYNRNFCRCPTTAE (SEQ ID NO:4 839-1032)	1032
MOUSE	1019	HFYNRNFCRCPTTAE (SEQ ID NO:6 840-1032)	1032
CAT	1017	HFYNRNFCRCPTTAE (SEQ ID NO:8 839-1031)	1031
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